

4 nucleic - nucleic search, using sw model							
Run on:	May 11, 2002, 14:53:54 ;	Search time	54.98 Seconds				
(without alignments)				8774.540 Million cell updates/sec			
Title:	US-09-911-513-1						
perfect score:	1964	1	taataatcattttttttctt.....tcttaaattactcacactggc 1964				
Sequence:	1						
Scoring table:	IDENTITY_NUC						
Gapop:	10.0		Gapext 1.0				
Searched:	383533 seqs,	12816752 residues					
Total number of hits satisfying chosen parameters:	767066						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	Issued_Patents_NA:*						
	1: /cgn2-6/ptfootdata/2/ina/5A..COMB.seq:*						
	2: /cgn2-6/ptfootdata/2/ina/5B..COMB.seq:*						
	3: /cgn2-6/ptfootdata/2/ina/5A..COMB.seq:*						
	4: /cgn2-6/ptfootdata/2/ina/6B..COMB.seq:*						
	5: /cgn2-6/ptfootdata/2/ina/5CTUS..COMB.seq:*						
	6: /cgn2-6/ptfootdata/2/ina/backfill1.seq:*						
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
8							
result No.	Score	Query Match	Length	DB ID	Description		
1	1964	100.0	1964	4 US-09-117-853-1	Sequence 1, Appli		
2	1580.4	80.5	1643	4 US-09-117-853-3	Sequence 2, Appli		
3	1570.4	79.9	1642	4 US-09-117-853-5	Sequence 3, Appli		
4	1570.0	79.9	1642	4 US-09-117-853-9	Sequence 4, Appli		
5	1556.4	79.2	1636	4 US-09-117-853-7	Sequence 5, Appli		
6	40.0	2.0	7218	1 US-08-232-463-14	Sequence 6, Appli		
7	37.6	1.9	7218	1 US-08-232-463-14	Sequence 7, Appli		
8	35.8	1.8	2372	1 US-09-145-391-1	Sequence 8, Appli		
9	35.4	1.8	2065	4 US-09-370-473-5	Sequence 9, Appli		
10	35.2	1.8	709	4 US-09-328-111-286	Sequence 10, Appli		
11	35.2	1.8	3441	4 US-08-896-164-85	Sequence 11, Appli		
12	34.2	1.7	796	1 US-08-104-073-2	Sequence 12, Appli		
13	34.0	1.7	1930	4 US-09-352-159-39	Sequence 13, Appli		
14	33.8	1.7	2160	4 US-09-386-607-1	Sequence 14, Appli		
15	33.2	1.7	760	4 US-08-896-164-59	Sequence 15, Appli		
16	33.2	1.7	3381	4 US-09-009-119-1	Sequence 16, Appli		
17	33.2	1.7	3381	4 US-09-371-507-1	Sequence 17, Appli		
18	33.2	1.7	3383	5 PCT-US95-09098-1	Sequence 18, Appli		
19	33.2	1.7	43676	3 US-09-356-952-12	Sequence 19, Appli		
20	33.0	1.7	1389	4 US-09-352-159-5	Sequence 20, Appli		
21	33.0	1.7	1389	4 US-09-352-168-5	Sequence 21, Appli		
22	33.0	1.7	1392	4 US-09-352-159-10	Sequence 22, Appli		
23	33.0	1.7	1392	4 US-09-352-168-10	Sequence 23, Appli		
24	33.0	1.7	1442	4 US-09-352-168-7	Sequence 24, Appli		
25	33.0	1.7	1442	4 US-09-352-168-7	Sequence 25, Appli		
26	33.0	1.7	1464	4 US-09-352-159-20	Sequence 26, Appli		
27	33.0	1.7	1464	4 US-09-352-168-30	Sequence 27, Appli		

NAME/KEY: misc_feature
 LOCATION: (648)..(688)
 OTHER INFORMATION: n = A, T, C or G
 US-09-352-159-39

RESULT 15
 US-08-896-164-59
 Sequence 59, Application US/08896164
 ; Patient No. 6218521
 ; GENERAL INFORMATION:
 ; APPLICANT: OBATA, Yuichi
 ; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
 ; WITH GASTRIC CANCER AND METHODS FOR
 ; TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
 ; NUMBER OF SEQUENCES: 87
 ; DIAGNOSING AND TREATING GASTRIC CANCER
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Feile & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/896,164
 ; FILING DATE: July 17, 1997
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6218521man D. Hanson
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LOD 5499 - JEL/NDH/SLH
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 638-3884
 ; INFORMATION FOR SEQ ID NO: 59:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 760 base pairs
 ; TYPE: nucleic acid
 ; SPANDEDNESS: double
 ; TOPOLOGY: linear
 ; US-08-896-164-59

Query Match 1.7%; Score 34; DB 4; Length 1930;
 Best Local Similarity 45.7%; Pred. No. 1;
 Matches 118; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
 Db 808 ttctccaaatcggtggccatcaaactgttccaaagaacatttccctgtgggg 8644
 ;

Query Match 1.7%; Score 33.8; DB 4; Length 2160;
 Best Local Similarity 55.6%; Pred. No. 1; 3;
 Matches 65; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
 Db 1388 attttactgtggtagccatggaaatcgatataatgtccgatttttagatcg 1444
 ;

RESULT 14
 US-09-386-607-1
 ; Sequence 1, Application US/09386607
 ; Patent No. 6162628
 ; GENERAL INFORMATION:
 ; APPLICANT: Cherry, Joel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Beier, Lars
 ; APPLICANT: Frandsen, Torben
 ; TITLE OF INVENTION: Maltotogenic Alpha-Amylase Variants
 ; FILE REFERENCE: 543.4.14-US
 ; CURRENT APPLICATION NUMBER: US/09/386,607
 ; CURRENT FILING DATE: 1999-08-31
 ; EARLIER APPLICATION NUMBER: DK98/00269
 ; EARLIER FILING DATE: 1998-02-27
 ; EARLIER APPLICATION NUMBER: 60/077,795
 ; EARLIER FILING DATE: 1998-03-12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2160
 ; TYPE: DNA
 ; ORGANISM: Bacillus sp.
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2160)
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: (100)..(2157)
 ; US-09-386-607-1

Query Match 1.7%; Score 33.2; DB 4; Length 760;
 Best Local Similarity 59.5%; Pred. No. 0; 98;
 Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 608 ATTCCCTCAAAATCTAAACCTTGAACTGATATGAGAAGAAACCCNTCCAGAAAGAAA
 ;

Query Match 1.7%; Score 33.2; DB 4; Length 760;
 Best Local Similarity 59.5%; Pred. No. 0; 98;
 Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 668 ACTCNANTCANAATGAAAAAAC 691
 ;

Query Match 1.7%; Score 33.2; DB 4; Length 760;
 Best Local Similarity 59.5%; Pred. No. 0; 98;
 Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 608 ATTCCCTCAAAATCTAAACCTTGAACTGATATGAGAAGAAACCCNTCCAGAAAGAAA
 ;

Query Match 1.7%; Score 33.2; DB 4; Length 760;
 Best Local Similarity 59.5%; Pred. No. 0; 98;
 Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Db 668 ACTCNANTCANAATGAAAAAAC 691
 ;

Search completed: May 11, 2002, 16:36:46
 Job time: 6172 sec